



PATENT DOCKET P0871P4D2

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of

Dan L. Eaton et al.

Serial No. 08/423,194

Filed: 18 April 1995

For: MPL LIGAND

Group Art Unit: 1812

Examiner: Unassigned

CERTIFICATE OF MAILING	
I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner of Patents and Trademarks, Washington, D.C. 20231 on	
September 8 1995	(Date of Deposit)
Elisa P. Hamby	Name of Depositing Party
Elisa P. Hamby	Signature of Depositing Party
9/8/95	Date of Signature

CERTIFICATE RE: SEQUENCE LISTING

BOX SEQUENCE

Honorable Commissioner of Patents  
and Trademarks  
Washington, D.C. 20231

Sir:

I hereby state that the Sequence Listing submitted herewith is submitted in paper copy and a computer-readable diskette, and that the content of the paper and computer readable copies are the same.

Respectfully submitted,

GENENTECH, INC.

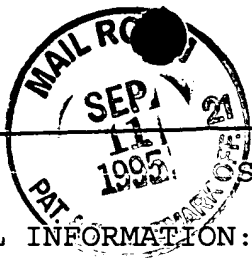
Date: September 8, 1995

By:

Daryl B. Winter

Reg. No. 32,637

460 Pt. San Bruno Blvd.  
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Phone: (415) 225-1249  
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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Eaton, Dan L.  
de Sauvage, Frederic J.
- (ii) TITLE OF INVENTION: MPL LIGAND
- 10 (iii) NUMBER OF SEQUENCES: 77
- (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 460 Point San Bruno Blvd  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080
- 20 (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: patin (Genentech)
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/423194  
(B) FILING DATE: 18-APR-1995  
30 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/249376  
(B) FILING DATE: 25-MAY-1994
- 35 (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/223263  
(B) FILING DATE: 04-APR-1994
- (vii) PRIOR APPLICATION DATA:  
40 (A) APPLICATION NUMBER: 08/196689  
(B) FILING DATE: 15-FEB-1994
- (vii) PRIOR APPLICATION DATA:  
45 (A) APPLICATION NUMBER: 08/185607  
(B) FILING DATE: 21-JAN-1994
- (vii) PRIOR APPLICATION DATA:  
50 (A) APPLICATION NUMBER: 08/176553  
(B) FILING DATE: 03-JAN-1994
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Winter, Daryl B.

(B) REGISTRATION NUMBER: 32,637  
(C) REFERENCE/DOCKET NUMBER: 871P4D2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-1249  
(B) TELEFAX: 415/952-9881  
(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr  
-21 -20 -15 -10  
Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu  
-5 1 5  
Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser  
10 15 20  
Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val  
25 30 35  
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln  
40 45 50  
Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu  
55 60 65  
Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr  
70 75 80  
Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu  
85 90 95  
Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro  
100 105 110  
Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu  
115 120 125  
Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu  
130 135 140  
Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr  
145 150 155

Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu  
160 165 170

5 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser  
175 180 185

Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe  
190 195 200

10 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu  
205 210 215

15 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn  
220 225 230

Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly  
235 240 245

20 Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro  
250 255 260

Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro  
265 270 275

Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr  
280 285 290

Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro  
295 300 305

30 Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His  
310 315 320

35 Ser Gln Asn Leu Ser Gln Glu Gly  
325 330 332

(2) INFORMATION FOR SEQ ID NO:2:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1795 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50

50 CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100

CCSCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150

5 CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200

GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250

10 TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300

ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350

15 AACTGAGCC AGTGCCCAGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT 400

20 GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450

CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500

25 ATGGCAGCAC GGGGACAACCT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550

GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600

30 TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650

AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700

35 CCTGATGCTT GTAGGAGGGT CCACCCTCTG CGTCAGGCGG GCCCCACCCA 750

40 CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800

CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850

45 AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAAGA 900

50 TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950

TACCTGAACA GGATACACGA ACTCTTGAAT GGAACTCGTG GACTCTTTCC 1000

TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTC TCAGGAACAT 1050  
 5 CAGACACAGG CTCCCTGCCA CCAACCTCC AGCCTGGATA TTCTCCTTCC 1100  
 CCAACCCATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150  
 10 CTTGCCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200  
 CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250  
 15 TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300  
 AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350  
 AACTGGACAA GATTTCTTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400  
 25 GGGATACACA GGA CTGAAAA GGAATCATT TTCTACTGTA CATTATAAAC 1450  
 CTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500  
 30 GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG ATTCTCTACA 1550  
 TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600  
 35 GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650  
 40 TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCATCC CCTTTACTAT 1700  
 CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750  
 45 AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA AAAAA 1795

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu  
-16 -15 -10 -5  
Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys  
1 5 10  
Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu  
15 20 25 26

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 390 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50  
CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT 100  
GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT 150  
CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA 200  
GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA 250  
CTCCCAGGAA GACACCATCA CTTCTCTTAA CTCCTTGACC CAATGACTAT 300  
TCTTCCCATA TTGTCCCCAC CTAAGTATCA CACTCTCTGA CAAGAATTAT 350  
TCTTCACAAT ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTAAGGACC TTATGGTCGA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA 50  
GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA 100  
CGTTC CGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA 150  
GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTCG TCTGACCACT 200  
CTTGAGGGTT GTAATAGGGG AAATAGGCGC ATTGACCATT CTGTGGGTAT 250  
GAGGGTCCTT CTGTGGTAGT GAAGGAGATT GAGGAACTGG GTTACTGATA 300  
AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA 350  
AGAAGTGTTA TGTCGGGCGT AAATTTTCGA GAGCAGATCT 390

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu  
1 5 10 15  
Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro  
20 25 30



	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	
					35					40					45	
5	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	
					50					55					60	
	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	
					65					70					75	
10	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	
					80					85					90	
	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	
					95					100					105	
15	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	
					110					115					120	
	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	
20					125					130					135	
	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	
					140					145					150	
	Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr	Ala	Val	Pro	Ser	Arg	Thr	
					155					160					165	
	Ser	Leu	Val	Leu	Thr	Leu	Asn	Glu	Leu	Pro	Asn	Arg	Thr	Ser	Gly	
					170					175					180	
30	Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser	Ala	Arg	Thr	Thr	Gly	Ser	
					185					190					195	
	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	Ile	Pro	Gly	
35					200					205					210	
	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	Asp	Gln	Ile	Pro	Gly	Tyr	
					215					220					225	
40	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	Gly	Thr	Arg	Gly	Leu	Phe	
					230					235					240	
	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	Ala	Pro	Asp	Ile	Ser	Ser	
					245					250					255	
45	Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	Pro	Asn	Leu	Gln	Pro	Gly	
					260					265					270	
	Tyr	Ser	Pro	Ser	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr	Thr	Leu	
50					275					280					285	

Sub  
B<sub>1</sub>  
C<sub>1</sub>

a'  
unk.

Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu His  
290 295 300

5 Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser  
305 310 315

Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln  
320 325 330

10 Glu Gly  
332

(2) INFORMATION FOR SEQ ID NO:7:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 166 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr  
1 5 10 15

25 Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala  
20 25 30

Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys  
35 40 45

Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala  
50 55 60

Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu  
65 70 75

Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro  
80 85 90

40 Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu  
95 100 105

Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser  
110 115 120

45 Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala  
125 130 135

Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg  
140 145 150

Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp  
155 160 165

Arg  
166

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu  
1 5 10 15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro  
20 25 30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp  
35 40 45

Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala  
50 55 60

Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met  
65 70 75

Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu  
80 85 90

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln  
95 100 105

Ser Leu Leu Gly Thr Gln Gly Arg Thr Thr Ala His Lys Asp Pro  
110 115 120

Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val  
125 130 135

Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg  
140 145 150

Ala Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu  
155 160 165

Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr  
170 175 180

Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys  
 185 190 195  
 5 Trp Gln Gln Gly Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln  
 200 205 210  
 Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile  
 215 220 225  
 10 His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser  
 230 235 240  
 Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp  
 245 250 255  
 15 Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser  
 260 265 270  
 20 Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro  
 275 280 285  
 Pro Thr Leu Pro Thr Pro Val Val Gln Leu His Pro Leu Leu Pro  
 290 295 300  
 25 Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn  
 305 310 315  
 Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu Gly  
 320 325 328

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

40 Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu  
 1 5 10 15  
 Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro  
 20 25 30  
 45 Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp  
 35 40 45  
 50 Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala  
 50 55 60

Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met  
 65 70 75  
 5 Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu  
 80 85 90  
 Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln  
 95 100 105  
 10 Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala  
 110 115 120  
 His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu  
 125 130 135  
 15 Arg Gly Lys Asp Phe Trp Ile Val Gly Asp Lys Leu His Cys Leu  
 140 145 150  
 20 Ser Gln Asn Tyr Trp Leu Trp Ala Ser Glu Val Ala Ala Gly Ile  
 155 160 165  
 Gln Ser Gln Asp Ser Trp Ser Ala Glu Pro Asn Leu Gln Val Pro  
 170 175 180  
 Gly Pro Asn Pro Arg Ile Pro Glu Gln Asp Thr Arg Thr Leu Glu  
 185 190 195  
 Trp Asn Ser Trp Thr Leu Ser Trp Thr Leu Thr Gln Asp Pro Arg  
 200 205 210  
 30 Ser Pro Gly His Phe Leu Arg Asn Ile Arg His Arg Leu Pro Ala  
 215 220 225  
 Thr Gln Pro Pro Ala Trp Ile Phe Ser Phe Pro Asn Pro Ser Ser  
 230 235 240  
 35 Tyr Trp Thr Val Tyr Ala Leu Pro Ser Ser Thr His Leu Ala His  
 245 250 255  
 40 Pro Cys Gly Pro Ala Pro Pro Pro Ala Ser  
 260 265

(2) INFORMATION FOR SEQ ID NO:10:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 261 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	
	1				5					10					15	
5	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	
					20					25					30	
	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	
					35					40					45	
10	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	
					50					55					60	
	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	
					65					70					75	
15	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	
					80					85					90	
	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	
20					95					100					105	
	Ser	Leu	Leu	Gly	Thr	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	
					110					115					120	
25	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Asp	
					125					130					135	
	Phe	Trp	Ile	Val	Gly	Asp	Lys	Leu	His	Cys	Leu	Ser	Gln	Asn	Tyr	
					140					145					150	
30	Trp	Leu	Trp	Ala	Ser	Glu	Val	Ala	Ala	Gly	Ile	Gln	Ser	Gln	Asp	
					155					160					165	
	Ser	Trp	Ser	Ala	Glu	Pro	Asn	Leu	Gln	Val	Pro	Gly	Pro	Asn	Pro	
35					170					175					180	
	Arg	Ile	Pro	Glu	Gln	Asp	Thr	Arg	Thr	Leu	Glu	Trp	Asn	Ser	Trp	
					185					190					195	
40	Thr	Leu	Ser	Trp	Thr	Leu	Thr	Gln	Asp	Pro	Arg	Ser	Pro	Gly	His	
					200					205					210	
	Phe	Leu	Arg	Asn	Ile	Arg	His	Arg	Leu	Pro	Ala	Thr	Gln	Pro	Pro	
					215					220					225	
45	Ala	Trp	Ile	Phe	Ser	Phe	Pro	Asn	Pro	Ser	Ser	Tyr	Trp	Thr	Val	
					230					235					240	
	Tyr	Ala	Leu	Pro	Ser	Ser	Thr	His	Leu	Ala	His	Pro	Cys	Gly	Pro	
50					245					250					255	

Sub  
B  
cont  
a  
cont.

Ala Pro Pro Pro Ala Ser  
260 261

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGTCCTTGG CCCAGCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50  
AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100  
ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG 150  
ATTTGCTCCT GCGGGCCATG CTCTTGCAG TGGCAAGACT AACTCTGTCC 200  
AGCCCCGTAG CTCCTGCCTG TGACCCAGA CTCCTAAATA AACTGCTGCG 250  
TGACTIONCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC 300  
CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA 350  
TGGAACACCC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT 400  
GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGCACAG TTGGAACCCT 450  
CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC 500  
TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGGGCAGGA CCACAGCTCA 550  
CAAGGACCCC AATGCCCTCT TCTTGAGCTT GCAACAACCTG CTTGGGGGAA 600  
AGGTGCGCTT CCTGCTTCTG GTAGAAGGTC CCACCCTCTG TGTACACG 650

ACCCTGCCAA CCACAGCTGT CCCAAGCAGT ACTTCTCAAC TCCTCACACT 700  
 AAACAAGTTC CCAAACAGGA CTTCTGGATT GTTGGAGACG AACTTCAGTG 750  
 TCACAGCCAG AACTGCTGGC CCTGGACTTC TGAGCAGGCT TCAGGGATTG 800  
 AGAGTCAAGA TTACTCCTGG TCAGCTAAAT CAAACCTCCA GGTCCCCAGT 850  
 CCAAATCTCT GGATACCTGA ACAGGACACA CGGACCTGTG AATGGAAGTC 900  
 ATGGGCTCTT TGCTGGAACC TCACTTCAGA CCCTGGAAGC CTCAGACATC 950  
 TCGCCCGGAG CTTTCAACAA AGGCTCCCTG GCATTCAACC TCCAGGGTGG 1000  
 ACTTCCTCCT TCTCCAAGCC TTGCTCCTGA TGGACACACA CCCTTCCCTC 1050  
 CTTACCTGC CTTGCCCACC ACCCATGGAT CTCCACCCCA GCTCCACCCC 1100  
 CTGTTTCCTG ACCCTTCCAC CACCATGCCT AACTCTACCG CCCCTCATCC 1150  
 AGTCACAATG TACCCTCATC CCAGGAATTT GTCTCAGGAA ACATAGCGCG 1200  
 GGCAGTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC AAGCTTCCCC 1250  
 AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTTCT GCTTTCACCT 1300  
 AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT AAAATTTTAG 1350  
 GAGCTATTTT TTTTAACTT ATCAGCAATA TTCATCAGAG CAGCTAGCGA 1400  
 TCTTTGGTCT ATTTTCGGTA TAAATTGAA AATCACTAAT TCT 1443

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 352 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val  
-21 -20 -15 -10

10 Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro  
-5 1 5

Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser  
10 15 20

15 Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val  
25 30 35

20 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln  
40 45 50

Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu  
55 60 65

25 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser  
70 75 80

30 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu  
85 90 95

Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Gly Arg Thr  
100 105 110

35 Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln  
115 120 125

Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro  
130 135 140

40 Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser  
145 150 155

Ser Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr  
160 165 170

45 Ser Gly Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala  
175 180 185

50 Gly Pro Gly Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile  
190 195 200

Thr Pro Gly Gln Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile  
 205 210 215  
 Ser Gly Tyr Leu Asn Arg Thr His Gly Pro Val Asn Gly Thr His  
 220 225 230  
 Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr Leu Glu Ala Ser Asp  
 235 240 245  
 Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu  
 250 255 260  
 Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His  
 265 270 275  
 Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly Ser  
 280 285 290  
 Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr Met  
 295 300 305  
 Pro Asn Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro  
 310 315 320  
 Arg Asn Leu Ser Gln Glu Thr  
 325 330 331

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1536 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50  
 AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100  
 ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG 150  
 ATTTGCTCCT GGC GGCCATG CTTCTTGCAG TGGCAAGACT AACTCTGTCC 200  
 AGCCCCGTAG CTCCTGCCTG TGACCCCAAGA CTCCTAAATA AACTGCTGCG 250

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TGACTCCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC 300  
CTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA 350  
TGGAAAACC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT 400  
GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCCT 450  
CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC 500  
TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGCTTCCTC TACAGGGCAG 550  
GACCACAGCT CACAAGGACC CCAATGCCCT CTTCTTGAGC TTGCAACAAC 600  
TGCTTCGGGG AAAGGTGCGC TTCCTGCTTC TGGTAGAAGG TCCCACCCTC 650  
TGTGTCAGAC GGACCCTGCC AACCACAGCT GTCCCAAGCA GTACTTCTCA 700  
ACTCCTCACA CTAAACAAGT TCCCAAACAG GACTTCTGGA TTGTTGGAGA 750  
CGAACTTCAG TGTCACAGCC AGAACTGCTG GCCCTGGACT TCTGAGCAGG 800  
CTTCAGGGAT TCAGAGTCAA GATTACTCCT GGTCAGCTAA ATCAAACCTC 850  
CAGGTCCCCA GTCCAAATCT CTGGATACCT GAACAGGACA CACGGACCTG 900  
TGAATGGAAC TCATGGGCTC TTTGCTGGAA CCTCACTTCA GACCCTGGAA 950  
GCCTCAGACA TCTCGCCCGG AGCTTTCAAC AAAGGCTCCC TGGCATTCAA 1000  
CCTCCAGGGT GGAATTCTC CTTCTCCAAG CCTTGCTCCT GATGGACACA 1050  
CACCTTCCC TCCTTCACCT GCCTTGCCCA CCACCCATGG ATCTCCACCC 1100  
CAGCTCCACC CCCTGTTTCC TGACCCTTCC ACCACCATGC CTAACCTCTAC 1150

CCCCCTCAT CCAGTCACAA TGTACCCTCA TCCCAGGAAT TTGTCTCAGG 1200  
 5 AAACATAGCG CGGGCACTGG CCCAGTGAGC GTCTGCAGCT TCTCTCGGGG 1250  
 ACAAGCTTCC CCAGGAAGGC TGAGAGGCAG CTGCATCTGC TCCAGATGTT 1300  
 10 CTGCTTTCAC CTAAAAGGCC CTGGGGAAGG GATACACAGC ACTGGAGATT 1350  
 GTAAAATTTT AGGAGCTATT TTTTTTTAAC CTATCAGCAA TATTCATCAG 1400  
 15 AGCAGCTAGC GATCTTTGGT CTATTTTCGG TATAAATTTG AAAATCACTA 1450  
 20 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 1536

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val  
 -21 -20 -15 -10  
 Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro  
 -5 1 5  
 Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser  
 10 15 20  
 Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val  
 25 30 35  
 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln  
 40 45 50  
 Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu  
 55 60 65

	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Glu	Pro	Ser
	70					75					80				
5	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu
	85					90					95				
	Leu	Leu	Gly	Ala	Leu	Gln	Gly	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Leu
	100					105					110				
10	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Leu	Phe	Leu
	115					120					125				
	Ser	Leu	Gln	Gln	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Leu	Leu
	130					135					140				
15	Val	Glu	Gly	Pro	Thr	Leu	Cys	Val	Arg	Arg	Thr	Leu	Pro	Thr	Thr
	145					150					155				
	Ala	Val	Pro	Ser	Ser	Thr	Ser	Gln	Leu	Leu	Thr	Leu	Asn	Lys	Phe
20	160					165					170				
	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	Asn	Phe	Ser	Val	Thr
	175					180					185				
25	Ala	Arg	Thr	Ala	Gly	Pro	Gly	Leu	Leu	Ser	Arg	Leu	Gln	Gly	Phe
	190					195					200				
	Arg	Val	Lys	Ile	Thr	Pro	Gly	Gln	Leu	Asn	Gln	Thr	Ser	Arg	Ser
	205					210					215				
30	Pro	Val	Gln	Ile	Ser	Gly	Tyr	Leu	Asn	Arg	Thr	His	Gly	Pro	Val
	220					225					230				
	Asn	Gly	Thr	His	Gly	Leu	Phe	Ala	Gly	Thr	Ser	Leu	Gln	Thr	Leu
35	235					240					245				
	Glu	Ala	Ser	Asp	Ile	Ser	Pro	Gly	Ala	Phe	Asn	Lys	Gly	Ser	Leu
	250					255					260				
40	Ala	Phe	Asn	Leu	Gln	Gly	Gly	Leu	Pro	Pro	Ser	Pro	Ser	Leu	Ala
	265					270					275				
	Pro	Asp	Gly	His	Thr	Pro	Phe	Pro	Pro	Ser	Pro	Ala	Leu	Pro	Thr
	280					285					290				
45	Thr	His	Gly	Ser	Pro	Pro	Gln	Leu	His	Pro	Leu	Phe	Pro	Asp	Pro
	295					300					305				
	Ser	Thr	Thr	Met	Pro	Asn	Ser	Thr	Ala	Pro	His	Pro	Val	Thr	Met
50	310					315					320				

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Tyr Pro His Pro Arg Asn Leu Ser Gln Glu Thr  
325 330 335

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser	Pro	Val	Ala	Pro	Ala	Cys	Asp	Pro	Arg	Leu	Leu	Asn	Lys	Leu
1				5					10					15
Leu	Arg	Asp	Ser	His	Leu	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro
				20					25					30
Asp	Val	Asp	Pro	Leu	Ser	Ile	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp
				35					40					45
Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Thr	Glu	Gln	Ser	Lys	Ala
				50					55					60
Gln	Asp	Ile	Leu	Gly	Ala	Val	Ser	Leu	Leu	Leu	Glu	Gly	Val	Met
				65					70					75
Ala	Ala	Arg	Gly	Gln	Leu	Glu	Pro	Ser	Cys	Leu	Ser	Ser	Leu	Leu
				80					85					90
Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln
				95					100					105
Gly	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Leu	Gln	Gly	Arg	Thr	Thr	Ala
				110					115					120
His	Lys	Asp	Pro	Asn	Ala	Leu	Phe	Leu	Ser	Leu	Gln	Gln	Leu	Leu
				125					130					135
Arg	Gly	Lys	Asp	Phe	Trp	Ile	Val	Gly	Asp	Glu	Leu	Gln	Cys	His
				140					145					150
Ser	Gln	Asn	Cys	Trp	Pro	Trp	Thr	Ser	Glu	Gln	Ala	Ser	Gly	Ile
				155					160					165
Gln	Ser	Gln	Asp	Tyr	Ser	Trp	Ser	Ala	Lys	Ser	Asn	Leu	Gln	Val
				170					175					180
Pro	Ser	Pro	Asn	Leu	Trp	Ile	Pro	Glu	Gln	Asp	Thr	Arg	Thr	Cys
				185					190					195

Glu Trp Asn Ser Trp Ala Leu Cys Trp Asn Leu Thr Ser Asp Pro  
200 205 210

5 Gly Ser Leu Arg His Leu Ala Arg Ser Phe Gln Gln Arg Leu Pro  
215 220 225

Gly Ile Gln Pro Pro Gly Trp Thr Ser Ser Phe Ser Lys Pro Cys  
230 235 240

10 Ser  
241

(2) INFORMATION FOR SEQ ID NO:16:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 335 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Pro Val Ala Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu  
1 5 10 15

25 Leu Arg Asp Ser His Leu Leu His Ser Arg Leu Ser Gln Cys Pro  
20 25 30

Asp Val Asp Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp  
35 40 45

30 Phe Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys Ala  
50 55 60

Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu Gly Val Met  
65 70 75

35 Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys Leu Ser Ser Leu Leu  
80 85 90

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln  
95 100 105

Gly Leu Leu Gly Thr Gln Leu Pro Leu Gln Gly Arg Thr Thr Ala  
110 115 120

45 His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln Leu Leu  
125 130 135

50 Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro Thr Leu  
140 145 150

Cys Val Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser Ser Thr  
 155 160 165  
 5 Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly  
 170 175 180  
 Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro  
 185 190 195  
 10 Gly Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile Thr Pro  
 200 205 210  
 Gly Gln Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile Ser Gly  
 215 220 225  
 15 Tyr Leu Asn Arg Thr His Gly Pro Val Asn Gly Thr His Gly Leu  
 230 235 240  
 Phe Ala Gly Thr Ser Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser  
 245 250 255  
 20 Pro Gly Ala Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly  
 260 265 270  
 25 Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His Thr Pro  
 275 280 285  
 Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly Ser Pro Pro  
 290 295 300  
 30 Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr Met Pro Asn  
 305 310 315  
 Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro Arg Asn  
 320 325 330  
 35 Leu Ser Gln Glu Thr  
 335

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu  
 1 5 10 15



	Leu	Arg	Asp	Ser	His	Val	Leu	His	Gly	Arg	Leu	Ser	Gln	Cys	Pro
					20					25					30
5	Asp	Ile	Asn	Pro	Leu	Ser	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp
					35					40					45
	Phe	Thr	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Thr	Glu	Gln	Thr	Lys	Ala
					50					55					60
10	Gln	Asp	Val	Leu	Gly	Ala	Thr	Thr	Leu	Leu	Leu	Glu	Ala	Val	Met
					65					70					75
	Thr	Ala	Arg	Gly	Gln	Val	Gly	Pro	Pro	Cys	Leu	Ser	Ser	Leu	Leu
					80					85					90
15	Val	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln
					95					100					105
20	Asp	Leu	Leu	Gly	Met	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala
					110					115					120
	His	Lys	Asp	Pro	Ser	Ala	Ile	Phe	Leu	Asn	Phe	Gln	Gln	Leu	Leu
					125					130					135
25	Arg	Gly	Lys	Val	Arg	Phe	Leu	Leu	Leu	Val	Val	Gly	Pro	Ser	Leu
					140					145					150
	Cys	Ala	Lys	Arg	Ala	Pro	Pro	Ala	Ile	Ala	Val	Pro	Ser	Ser	Thr
					155					160					165
30	Ser	Pro	Phe	His	Thr	Leu	Asn	Lys	Leu	Pro	Asn	Arg	Thr	Ser	Gly
					170					175					180
	Leu	Leu	Glu	Thr	Asn	Ser	Ser	Ile	Ser	Ala	Arg	Thr	Thr	Gly	Ser
					185					190					195
	Gly	Phe	Leu	Lys	Arg	Leu	Gln	Ala	Phe	Arg	Ala	Lys	Ile	Pro	Gly
					200					205					210
	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	Asp	Gln	Ile	Pro	Gly	His
					215					220					225
	Gln	Asn	Gly	Thr	His	Gly	Pro	Leu	Ser	Gly	Ile	His	Gly	Leu	Phe
					230					235					240
45	Pro	Gly	Pro	Gln	Pro	Gly	Ala	Leu	Gly	Ala	Pro	Asp	Ile	Pro	Pro
					245					250					255
	Ala	Thr	Ser	Gly	Met	Gly	Ser	Arg	Pro	Thr	Tyr	Leu	Gln	Pro	Gly
50					260					265					270

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Glu Ser Pro Ser Pro Ala His Pro Ser Pro Gly Arg Tyr Thr Leu  
275 280 285

Phe Ser Pro Ser Pro Thr Ser Pro Ser Pro Thr Val Gln Leu Gln  
290 295 300

Pro Leu Leu Pro Asp Pro Ser Ala Ile Thr Pro Asn Ser Thr Ser  
305 310 315

Pro Leu Leu Phe Ala Ala His Pro His Phe Gln Asn Leu Ser Gln  
320 325 330

Glu Glu  
332

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGCCCGGCTC CTCCTGCCTG TGACCCCCGA CTCCTAAATA AACTGCTTCG 50  
TGACTCCCAT GTCCTTCACG GCAGACTGAG CCAGTGCCCA GACATTAACC 100  
CTTGTGCCAC ACCTGTCCTG CTGCCTGCTG TGGACTTCAC CTTGGGAGAA 150  
TGGAACCC AGACGGAGCA GACAAAGGCA CAGGATGTCC TGGGAGCCAC 200  
AACCCTTCTG CTGGAGGCAG TGATGACAGC ACGGGGACAA GTGGGACCCC 250  
CTTGCCTCTC ATCCCTGCTG GTGCAGCTTT CTGGACAGGT TCGCCTCTC 300  
CTCGGGGCC TGCAGGACCT CTTGGAATG CAGCTTCCTC CACAGGGAAG 350  
GACCACAGCT CACAAGGATC CCAGTGCCAT CTTCTGAAC TTCCAACAAC 400  
TGCTCCGAGG AAAGGTGCGT TTCCTGCTCC TTGTAGTGGG GCCCTCCCTC 450

TGTGCCAAGA GGGCCCCACC CGCCATAGCT GTCCCGAGCA GCACCTCTCC 500  
 ATTCCACACA CTGAACAAGC TCCCAAACAG GACCTCTGGA TTGTTGGAGA 550  
 CAAACTCCAG TATCTCAGCC AGAACTACTG GCTCTGGATT TCTCAAGAGG 600  
 CTGCAGGCAT TCAGAGCCAA GATTCCTGGT CTGCTGAACC AAACCTCCAG 650  
 GTCCCTAGAC CAAATCCCTG GACACCAGAA TGGGACACAC GGACCCTTGA 700  
 GTGGAATTCA TGGACTCTTT CCTGGACCCC AACCCGGGGC CCTCGGAGCT 750  
 CCAGACATTC CTCCAGCAAC TTCAGGCATG GGCTCCCGGC CAACCTACCT 800  
 CCAGCCTGGA GAGTCTCCTT CCCAGCTCA CCCTTCTCCT GGACGATACA 850  
 CTCTCTTCTC TCCTTCACCC ACCTCGCCCT CCCCCACAGT CCAGCTCCAG 900  
 CCTCTGCTTC CTGACCCCTC TGCATCACA CCCAACTCTA CCAGTCCTCT 950  
 TCTATTTGCA GCTCACCTC ATTTCCAGAA CCTGTCTCAG GAAGAGTAAG 1000  
 GTGCTCAGAC CCGCCAACT TCAGCA 1026

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCCCGGCTC CTCCTGCCTG TGACCCCGGA CTCCTAAATA AACTGCTTCG 50  
 TGACTCCCAT GTCCTTCACG GCAGACTGAG CCAGTGCCCA GACATTAACC 100

~~CTTTGTCCAC ACCTGTCCTG CTGCCTGCTG TGGACTTCAC CTTGGGAGAA 150  
 5 TGGAAAACCC AGACGGAGCA GACAAAGGCA CAGGATGTCC TGGGAGCCAC 200  
 AACCCCTTCTG CTGGAGGCAG TGATGACAGC ACGGGGACAA GTGGGACCCC 250  
 10 CTTGCCTCTC ATCCCTGCTG GTGCAGCTTT CTGGACAGGT TCGCCTCCTC 300  
 CTCGGGGCCC TGCAGGACCT CCTTGGAATG CAGGGAAGGA CCACAGCTCA 350  
 15 CAAGGATCCC AGTGCCATCT TCCTGAACTT CCAACAACCTG CTCCGAGGAA 400  
 20 AGGTGCGTTT CCTGCTCCTT GTAGTGGGGC CCTCCCTCTG TGCCAAGAGG 450  
 GCCCCACCCG CCATAGCTGT CCCGAGCAGC ACCTCTCCAT TCCACACACT 500  
 25 GAACAAGCTC CCAAACAGGA CCTCTGGATT GTTGGAGACA AACTCCAGTA 550  
 TCTCAGCCAG AACTACTGGC TCTGGATTTC TCAAGAGGCT GCAGGCATTC 600  
 30 AGAGCCAAGA TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTAGACCA 650  
 AATCCCTGGA CACCAGAATG GGACACACGG ACCCTTGAGT GGAATTCATG 700  
 GACTCTTTCC TGGACCCCAA CCCGGGGCCC TCGGAGCTCC AGACATTCCT 750  
 CCAGCAACTT CAGGCATGGG CTCCCGGCCA ACCTACCTCC AGCCTGGAGA 800  
 GTCTCCTTCC CCAGCTCACC CTTCTCCTGG ACGATACTCT CTCTTCTCTC 850  
 45 CTTACCCAC CTCGCCCTCC CCCACAGTCC AGCTCCAGCC TCTGCTTCCT 900  
 50 GACCCCTCTG CGATCACACC CAACTCTACC AGTCCTCTTC TATTGTCAGC 950~~

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TCACCCTCAT TTCCAGAACC TGTCTCAGGA AGAGTAAGGT GCTCAGACCC 1000

TGCCAACTTC AGCA 1014

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(2) INFORMATION FOR SEQ ID NO:20:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu  
1 5 10 15

20

Leu Arg Asp Ser His Val Leu His Gly Arg Leu Ser Gln Cys Pro  
20 25 30

Asp Ile Asn Pro Leu Ser Thr Pro Val Leu Leu Pro Ala Val Asp  
35 40 45

25

Phe Thr Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Thr Lys Ala  
50 55 60

Gln Asp Val Leu Gly Ala Thr Thr Leu Leu Leu Glu Ala Val Met  
65 70 75

30

Thr Ala Arg Gly Gln Val Gly Pro Pro Cys Leu Ser Ser Leu Leu  
80 85 90

Val Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln  
95 100 105

Asp Leu Leu Gly Met Gln Gly Arg Thr Thr Ala His Lys Asp Pro  
110 115 120

Ser Ala Ile Phe Leu Asn Phe Gln Gln Leu Leu Arg Gly Lys Val  
125 130 135

Arg Phe Leu Leu Leu Val Val Gly Pro Ser Leu Cys Ala Lys Arg  
140 145 150

45

Ala Pro Pro Ala Ile Ala Val Pro Ser Ser Thr Ser Pro Phe His  
155 160 165

Thr Leu Asn Lys Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr  
170 175 180

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Asn Ser Ser Ile Ser Ala Arg Thr Thr Gly Ser Gly Phe Leu Lys  
 185 190 195  
 Arg Leu Gln Ala Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln  
 200 205 210  
 Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly His Gln Asn Gly Thr  
 215 220 225  
 His Gly Pro Leu Ser Gly Ile His Gly Leu Phe Pro Gly Pro Gln  
 230 235 240  
 Pro Gly Ala Leu Gly Ala Pro Asp Ile Pro Pro Ala Thr Ser Gly  
 245 250 255  
 Met Gly Ser Arg Pro Thr Tyr Leu Gln Pro Gly Glu Ser Pro Ser  
 260 265 270  
 Pro Ala His Pro Ser Pro Gly Arg Tyr Thr Leu Phe Ser Pro Ser  
 275 280 285  
 Pro Thr Ser Pro Ser Pro Thr Val Gln Leu Gln Pro Leu Leu Pro  
 290 295 300  
 Asp Pro Ser Ala Ile Thr Pro Asn Ser Thr Ser Pro Leu Leu Phe  
 305 310 315  
 Ala Ala His Pro His Phe Gln Asn Leu Ser Gln Glu Glu  
 320 325 328

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu  
 1 5 10 15  
 Leu Arg Asp Asp His Val Leu His Gly Arg  
 20 25

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu  
1 5 10 15

Leu Arg Asp Asp His Ser Val Leu His Gly Arg Leu  
20 25 27

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu  
1 5 10 15

Leu Arg Asp Asp His Val Leu His Gly Arg  
20 25

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys  
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Pro Arg Leu Leu Asn Lys Leu Leu Arg  
1 5 9

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCNGCNCNC CNGCNTGYGA 20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

NCCRTGNARN ACRTGRTCRT C 21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50



TGACCACGTT CAGCACGGC 69

5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

15

GCCGTGCTGA ACGTGGTCAT CACGAGGCAG TTTATTTAGG AGTCGGGGGT 50

20

CACAGGCTGG CGGCGCTGG 69

(2) INFORMATION FOR SEQ ID NO:31:

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

35

CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

CGACCACGTC CATCACGGC 69

(2) INFORMATION FOR SEQ ID NO:32:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCCGTGATGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCGGGGGT 50

CACATGCCGG AGGTGCTGG 69

5

(2) INFORMATION FOR SEQ ID NO:33:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

20

CGATCATGTC TATCAAGGT 69

25

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

35

ACCGTGATAG ACATGATCGT CACGAAGCAG TTTATTTAGG AGTCGGGGGT 50

40

CACATGCCGG CGGTGCTGG 69

(2) INFORMATION FOR SEQ ID NO:35:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 22 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

15

CAGTCTGCCG TGAAGGACAT GG 22

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

30

TGTGGACTTT AGCTTGGGAG AATG 24

35

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 22 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

45

GGTCCAGGGA CCTGGAGGTT TG 22

50

(2) INFORMATION FOR SEQ ID NO:39:

Sub  
B1  
cont  
30  
cont.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATCGATATCG ATAGCCAGAC ACCCCGGCCA G 31

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCTAGCTCTA GACAGGGAAG GGAGCTGTAC ATGAGA 36

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTCCTTGGA CCCAGGGCAG GACC 24

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Sub  
B1  
cont  
a' cont.

GGTCCTGCCC TGGGTTCCAA GGAG 24

5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 27 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

15

CTGCTCCGAG GAAAGGACTT CTGGATT 27

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AATCCAGAAG TCCTTTCCTC GGAGCAG 27

35

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 28 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

45

CCCTCTGCGT CGCGGCGGCC CCACCCAC 28

50

(2) INFORMATION FOR SEQ ID NO:46:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTGGGTGGGG CCGCCGCGAC GCAGAGGG 28

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GACTCGAGGA TCCATCGATT TTTTTTTTTT TTTT 35

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GACTCGAGGA TCCATCG 17

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Sub  
B1  
cont  
a' 30  
cont.

GCTAGCTCTA GAAGCCCGGC TCCTCCTGCC TG 32

5

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGAAATTAAC CTCCTACTAAA G 21

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

30

His Val Leu His  
1 4

(2) INFORMATION FOR SEQ ID NO:52:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Arg Leu Ser  
1 4

45

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ser His Val Leu  
1 4

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

His Ser Arg Leu  
1 4

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Val Asp Phe  
1 4

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Leu Gly Glu  
1 4

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ala Val Thr Leu  
1 4

(2) INFORMATION FOR SEQ ID NO:58:



(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Leu Glu Gly  
1 4

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Leu Ser Ser Leu  
1 4

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Leu Gly Gln Leu  
1 4

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Cys Leu Ser Ser  
1 4

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Leu Leu Gly Gln

1 4

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ser Ser Leu Leu

1 4

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gly Gln Leu Ser

1 4

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Leu Gln Ser Leu

1 4

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Leu Gly Thr Gln

1 4

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ala Leu Gln Ser  
1 4

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Leu Leu Gly Thr  
1 4

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Asn Ala Ile Phe  
1 4

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Leu Ser Phe Gln  
1 4

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

5 Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu  
1 5 10 15  
10 Leu Arg Asp Ser His Val Leu  
20 22

(2) INFORMATION FOR SEQ ID NO:72:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

20 His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr  
1 5 10 15  
Sub B1 cont  
Pro Val Leu Leu Pro Ala Val Asp Phe  
20 24

(2) INFORMATION FOR SEQ ID NO:73:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
al cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

35 Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln  
1 5 10 15  
40 Asp Ile Leu Gly Ala Val Thr Leu  
20 23

(2) INFORMATION FOR SEQ ID NO:74:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

50 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr  
1 5 10 15

Cys Leu Ser Ser Leu Leu  
20 21

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln  
1 5 10 15  
Ser  
16

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His  
1 5 10 15  
Lys Asp Pro Asn Ala Ile Phe  
20 22

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met  
1 5 10 15  
Leu Val Gly Gly Ser Thr Leu Cys Val Arg  
20 25